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RAW SEQUENCE LISTING

DATE: 05/01/2002

PATENT APPLICATION: US/10/023,171

TIME: 12:01:29

Input Set : N:\Crf3\RULE60\10023171.raw

Output Set: N:\CRF3\05012002\J023171.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Weiner, Joel H.

6 Turner, Raymond J.

8 (ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTEIN

9 SECRETION

11 (iii) NUMBER OF SEQUENCES: 77

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Medlen & Carroll, LLP

15 (B) STREET: 220 Montgomery Street, Suite 2200

16 (C) CITY: San Francisco

17 (D) STATE: California

18 (E) COUNTRY: United States of America

19 (F) ZIP: 94104

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/10/023,171

C--> 29 (B) FILING DATE: 17-Dec-2001

30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: US/09/085,761

34 (B) FILING DATE: 28-MAY-1998

36 (viii) ATTORNEY/AGENT INFORMATION:

37 (A) NAME: Carroll, Peter G.

38 (B) REGISTRATION NUMBER: 32,837

39 (C) REFERENCE/DOCKET NUMBER: UALB-03356

41 (ix) TELECOMMUNICATION INFORMATION:

42 (A) TELEPHONE: (415) 705-8410

43 (B) TELEFAX: (415) 397-8338

46 (2) INFORMATION FOR SEQ ID NO: 1:

48 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 277 amino acids

50 (B) TYPE: amino acid

51 (C) STRANDEDNESS: Not Relevant

52 (D) TOPOLOGY: unknown

54 (ii) MOLECULE TYPE: protein

59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

61 Met Arg Leu Cys Leu Ile Ile Ile Tyr His Arg Gly Thr Cys Met Gly

62 1 5 10 15

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64   Gly Ile Ser  Ile Trp Gln Leu Leu Ile Ile Ala Val Ile Val Val Leu
65               20                25                30
67   Leu Phe Gly Thr Lys Lys Leu Gly Ser Ile Gly Ser Asp Leu Gly Ala
68               35                40                45
70   Ser Ile Lys Gly Phe Lys Lys Ala Met Ser Asp Asp Glu Pro Lys Gln
71               50                55                60
73   Asp Lys Thr Ser  Gln Asp Ala Asp Phe Thr Ala Lys Thr Ile Ala Asp
74               65                70                75                80
76   Lys Gln Ala Asp Thr Asn Gln Glu Gln Ala Lys Thr Glu Asp Ala Lys
77               85                90                95
79   Arg His Asp Lys Glu Gln Gly Val Asn Pro Cys Leu Ile Ser Val Leu
80               100               105               110
82   Ala Asn Leu Leu Leu Val Phe Ile Ile Gly Leu Val Val Leu Gly Pro
83               115               120               125
85   Gln Arg Leu Pro Val Ala Val Lys Thr Val Ala Gly Trp Ile Arg Ala
86               130               135               140
88   Leu Arg Ser Leu Ala Thr Thr Val Gln Asn Glu Leu Thr Gln Glu Leu
89               145               150               155               160
91   Lys Leu Gln Glu Phe Gln Asp Ser Leu Lys Lys Val Glu Lys Ala Ser
92               165               170               175
94   Leu Thr Asn Leu Thr Pro Glu Leu Lys Ala Ser Met Asp Glu Leu Arg
95               180               185               190
97   Gln Ala Ala Glu Ser Met Lys Arg Ser Tyr Val Ala Asn Asp Pro Glu
98               195               200               205
100   Lys Ala Ser Asp Glu Ala His Thr Ile His Asn Pro Val Val Lys Asp
101               210               215               220
103   Asn Glu Ala Ala His Glu Gly Val Thr Pro Ala Ala Ala Gln Thr Gln
104               225               230               235               240
106   Ala Ser Ser Pro Glu Gln Lys Pro Glu Thr Thr Pro Glu Pro Val Val
107               245               250               255
109   Lys Pro Ala Ala Asp Ala Glu Pro Lys Thr Ala Ala Pro Ser Pro Ser
110               260               265               270
112   Ser Ser Asp Lys Pro
113               275
115 (2) INFORMATION FOR SEQ ID NO: 2:
117   (i) SEQUENCE CHARACTERISTICS:
118       (A) LENGTH: 284 amino acids
119       (B) TYPE: amino acid
120       (C) STRANDEDNESS: Not Relevant
121       (D) TOPOLOGY: unknown
123   (ii) MOLECULE TYPE: protein
128   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
130   Met Ala Lys Lys Ser Ile Phe Arg Ala Lys Phe Phe Leu Phe Tyr Arg
131       1           5           10           15
133   Thr Glu Phe Ile Met Phe Gly Leu Ser Pro Ala Gln Leu Ile Ile Leu
134               20           25           30
136   Leu Val Val Ile Leu Leu Ile Phe Gly Thr Lys Lys Leu Arg Asn Ala
137               35           40           45
139   Gly Ser Asp Leu Gly Ala Ala Val Lys Gly Phe Lys Lys Ala Met Lys

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140          50          55          60
142      Glu Asp Glu Lys Val Lys Asp Ala Glu Phe Lys Ser Ile Asp Asn Glu
143      65          70          75          80
145      Thr Ala Ser Ala Lys Lys Gly Lys Tyr Lys Arg Glu Arg Asn Arg Leu
146          85          90          95
W--> 148      Asn Pro Cys Leu Ile Leu Val Phe Gln Asn Leu Phe Tyr Xaa Met Val
149          100          105          110
151      Leu Gly Leu Val Val Leu Gly Pro Lys Arg Leu Pro Ile Ala Ile Arg
152          115          120          125
154      Thr Val Met Asp Trp Val Lys Thr Ile Arg Gly Leu Ala Ala Asn Val
155          130          135          140
157      Gln Asn Glu Leu Lys Gln Glu Leu Lys Leu Gln Glu Leu Gln Asp Ser
158      145          150          155          160
160      Ile Lys Lys Ala Glu Ser Leu Asn Leu Gln Ala Leu Ser Pro Glu Leu
161          165          170          175
163      Ser Lys Thr Val Glu Glu Leu Lys Ala Gln Ala Asp Lys Met Lys Ala
164          180          185          190
166      Glu Leu Glu Asp Lys Ala Ala Gln Ala Gly Thr Thr Val Glu Asp Gln
167          195          200          205
169      Ile Lys Glu Ile Lys Ser Ala Ala Glu Asn Ala Glu Lys Ser Gln Asn
170          210          215          220
172      Ala Ile Ser Val Glu Glu Ala Ala Glu Thr Leu Ser Glu Ala Glu Arg
173      225          230          235          240
175      Thr Pro Thr Asp Leu Thr Ala Leu Glu Thr His Glu Lys Val Glu Leu
176          245          250          255
178      Asn Thr His Leu Ser Ser Tyr Tyr Pro Pro Asp Asp Ile Glu Ile Ala
179          260          265          270
181      Pro Ala Ser Lys Ser Gln Ser Ser Lys Thr Lys Ser
182          275          280

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184 (2) INFORMATION FOR SEQ ID NO: 3:

186 (i) SEQUENCE CHARACTERISTICS:

187 (A) LENGTH: 22108 base pairs

188 (B) TYPE: nucleic acid

189 (C) STRANDEDNESS: double

190 (D) TOPOLOGY: unknown

192 (ii) MOLECULE TYPE: DNA (genomic)

197 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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199 AGTCCTGCAG AATGAAGGGT GATTTATGTG ATTTGCATCA CTTTGGTG GGTAAATTTAT      60
201 GCAACGCATT TCGGTCATGG TGATGAGTAT CACGAAAAAA TGTTAAACCC TTCGGTAAAG      120
203 TGTCTTTTTG CTTCTTCTGA CTAAACCGAT TCACAGAGGA GTTGATATATG TCCAAGTCTG      180
205 ATGTTTTTCA TCTCGGCCCTC ACTAAAAACG ATTTACAAGG GGCTACGCTT GCCATCGTCC      240
207 CTGGCGACCC GGATCGTGTG GAAAAGATCG CCGCGCTGAT GGATAAGCCG GTTAAGCTGG      300
209 CATCTACCG CGAATTCAC TACCTGGCGTG CAGAGCTGGA TGGTAAACCT GTTATCGTCT      360
211 GCTCTACCG TATCGGCGGC CCGTCTACCT CTATTGCTGT TGAAGAGCTG GCACAGCTGG      420
213 GCATTCGCAC CTTCTGCGT ATCGGTACAA CGGGCGCTAT TCAGCCGCAT ATTAATGTGG      480
215 GTGATGTCCT GGTACCACG GCGTCTGTCC GTCTGGATGG CGCGAGCCTG CACTTCGCAC      540
217 CGCTGGAATT CCCGGCTGTC GCTGATTTTC AATGTACGAC TGCGCTGGTT GAAGCTGCGA      600
219 AATCCATTGG CGCGACAAC CACGTTGGCG TGACAGCTTC TTCTGATACC TTCTACCCAG      660
221 GTCAGGAACG TTACGATACT TACTCTGGTC GCGTAGTTTC TCACTTTAAA GGTTCATATG      720

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223	AAGAGTGGCA	GGCGATGGGC	GTAATGAACT	ATGAAATGGA	ATCTGCAACC	CTGCTGACCA	780
225	TGTGTGCAAG	TCAGGGCCTG	CGTGCCGGTA	TGGTAGCGGG	TGTTATCGTT	AACCCGACCCC	840
227	AGCAAGAGAT	CCCGAATGCT	GAGACGATGA	AACAAACCGA	AAGCCATGCG	GTGAAAAATCG	900
229	TGGTGGAAGC	GGCGCGTCGT	CTGCTGTAAT	TCTCTTCTCC	TGTCTGAAGG	CCGACGCGTT	960
231	CGGCCTTTTG	TATTTTTCG	TAGCGCCTCG	CAGGAAATGC	CTTTCCAAC	GGACGTTTGT	1020
233	ACAGCACAAT	TCTATTTTGT	GCGGGTAAGT	TGTTGCGTCA	GGAGGCGTTG	TGGATTTCTC	1080
235	AATCATGGTT	TACGCAGTTA	TTGCGTTGGT	GGGTGTGGCA	ATTGGCTGGC	TGTTTGCCAG	1140
237	TTATCAACAT	GCGCAGCAAA	AAGCCGAGCA	ATTAGCTGAA	CGTGAAGAGA	TGGTCGCGGA	1200
239	GTTAAGCGCG	GCAAAAACAAC	AAATTACCCA	AAGCGAGCAC	TGGCGTGCG	AGTGCGAGTT	1260
241	ACTCAATAAC	GAAGTGCGCA	GCCTGCAAA	TATTAACACC	TCTCTGGAGG	CCGATCTGCG	1320
243	TGAAGTAACC	ACGCGGATGG	AAGCCGCACA	GCAACATGCT	GACGATAAAA	TTCCGCCAGAT	1380
245	GATTAACAGC	GAGCAGCGCC	TCAGTGAGCA	GTTTGAAAAC	CTCGCCAACC	GTATTTTGA	1440
247	GCACAGCAAT	CGCCGGGTTG	ATGAGCAAAA	CCGTCAGAGT	CTGAACAGCC	TGTTGTCGCC	1500
249	GCTACGTGAA	CAACTGGACG	GTTTCCGCCG	TCAGGTTTCA	GACAGCTTCG	GTAAGAAGC	1560
251	ACAAGAACGC	CATACCCTGA	CCCACGAAAT	TCGCAATCTC	CAGCAACTCA	ACGCGCAAAT	1620
253	GGCCAGGAA	GCGATCAACC	TGACGCGCGC	GCTGAAAAGC	GACAATAAAA	CCCAGGGCAA	1680
255	CTGGGGCGAG	GTAGTATTGA	CGCGGGTGCT	GGAGGCTTCC	GGTCTGCGTG	AAGGGTATGA	1740
257	ATATGAAACC	CAGGTCAGCA	TCGAAAATGA	CGCCCCGCTC	CGGATGCAGC	CGGATGTCAT	1800
259	CGTGCGCCTG	CCGAGGGGAA	AAGATGTGGT	GATCGACGCC	AAAAATGACG	TGGTCGCCTA	1860
261	TGAACGCTAT	TTTAACGCCG	AAGACGACTA	CACCCGCGAA	AGCGCGCTAC	AGGAACATAT	1920
263	CGCGTCGGTG	CGTAACCAT	TCCGTTTGCT	GGGACGCAAA	GATTATCAAC	AGCTGCCGGG	1980
265	GCTCGGAATC	CTGGATTACG	TGCTGATGTT	TATTCCCGTT	GAACCCGCTT	TTTFACTGGC	2040
267	GCTTGACCGC	CAGCCGGAGC	TGATCACCGA	AGCGTTGAAA	AACAACATCA	TGCTGGTTAG	2100
269	CCCGACTACG	CTGCTGGTGG	CGCTGCGCAC	TATCGCCAAC	CTGTGGCGTT	ATGAGCATCA	2160
271	AAGCCGCAAC	GCCAGCAAAA	TCGCCGATCG	TGCCAGCAAG	CTGTACGACA	AGATGCGTTT	2220
273	GTTTCATCGAT	GACATGTCCG	CGATTGGTCA	AAGTCTCGAC	AAAGCGCAGG	ATAATTATCG	2280
275	GCAGGCAATG	AAAAAACTCT	CTTCAGGGCG	CGGAAATGTG	CTGGCGCAGG	CAGAAGCGTT	2340
277	TCGCGGTTTA	GGAGTAGAAA	TTAAACGCGA	GATTAAATCCG	GATTTGCGTG	AACAGGCGGT	2400
279	GAGCCAGGAT	GAAGAGTATC	GACTTCGGTC	GTTTCCGGAG	CAGCCGAATG	ATGAAGCTTA	2460
281	TCAACGCGAT	GATGAATATA	ATCAGCAGTC	GCGCTAGCCC	ATTGGGAGTA	GTTAAGCCGG	2520
283	GTAGAAATCT	AGGGCATCGA	CGCCCAATCT	GTTACACTTC	TGGAACAATT	TTTGTATGAG	2580
285	CAGGCATTGA	GATGGTGGAT	AAGTCACAA	AAACGACGCA	CTTTGGTTTT	CAGACCGTCG	2640
287	CGAAGGAACA	AAAAGCGGAT	ATGGTCGCCC	ACGTTTTTCCA	TTCCGTGGCA	TCAAAAATACG	2700
289	ATGTCATGAA	TGATTTGATG	TCATTTGGTA	TTTCATCGTTT	GTGGAAGCGA	TTACCGATTG	2760
291	ATTGCAGCGG	CGTACGCCGT	GGGCAGACCG	TGCTGGATCT	GGCTGGTGGC	ACCGGCGACC	2820
293	TGACAGCGAA	ATTCTCCCGC	CTGGTCGGAG	AAACTGGCAA	AGTGGTCCTT	GCTGATATCA	2880
295	ATGAATCCAT	GCCCAAAATG	GGCCGCAGAA	AGCTGCGTAA	TATCGGTGTG	ATTGGCAACG	2940
297	TTGAGTATGT	TCAGGCGAAC	GCTGAGGCGC	TGCCGTTCCC	GGATAACACC	TTTGATTGCA	3000
299	TCACCATTTT	GTTTGGTCTG	CGTAACGTCA	CCGACAAAGA	TAAAGCACTG	CGTTCAATGT	3060
301	ATCGCGTGCT	GAAACCCGGC	GGCCGCCTGC	TGGTGCTTGA	GTTCTCGAAG	CCAATTATCG	3120
303	AGCCGCTGAG	CAAAGCCTAT	GATGCATACT	CCTTCCATGT	GCTGCCGCGT	ATTGGCTCAC	3180
305	TGGTCGCGAA	CGACGCCGAC	AGCTACCGTT	ATCTGGCAGA	ATCCATCCGT	ATGCATCCCCG	3240
307	ATCAGGATAC	CCTGAAAGCC	ATGATGCAGG	ATGCCGGATT	CGAAAGTGTC	GACTIONTACA	3300
309	ATCTGACGGC	AGGGGTTGTG	GCGCTGCATC	GTGGTTATAA	GTTCTGACAG	GAGACCGGAA	3360
311	ATGCCTTTTA	AACCTTTAGT	GACGGCAGGA	ATTGAAAGTC	TGCTCAACAC	CTTCTGTGAT	3420
313	CGCTCACCCG	CGCTGAAAAC	GGCCCGCTCG	CGTCTGCTGG	GTAAAGTATT	GCGCGTGGAG	3480
315	GTAAAGGGCT	TTTCGACGTC	ATTGATTCTG	GTGTTACGCG	AACGCCAGGT	TGATGTACTG	3540
317	GGCGAATGGG	CAGGCGATGC	TGACTGCACC	GTTATCGCCT	ACGCCAGTGT	GTTGCCGAAA	3600
319	CTTCGCGATC	GCCAGCAGCT	TACCGCACTG	ATTCGCGAGT	GTGAGCTGGA	AGTGCGAGGG	3660

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321	GATATTCAGG	TGGTGCAAAA	CTTCGTTGCG	CTGGCAGATC	TGGCAGAGTT	CGACCCTGCG	3720
323	GAAC TGCTGG	CCCC TTATAC	CGGTGATATC	GCCGCTGAAG	GAATCAGCAA	AGCCATGCGC	3780
325	GGAGGCGCAA	AGTTCCTGCA	TCACGGCATT	AAGCGCCAGC	AACGTTATGT	GGCGGAAGCC	3840
327	ATTACTGAAG	AGTGGCGTAT	GGCACCCGGT	CCGCTTGAAG	TGGCCTGGTT	TGCGGAAGAG	3900
329	ACGGCTGCCG	TCGAGCGTGC	TGTTGATGCC	CTGACCAAA	GGCTGGA AAA	ACTGGAGGCT	3960
331	AAATGACGCC	AGGTGAAGTA	CGGCGCCTAT	ATTTTCATCAT	TCGCACTTTT	TTAAGCTACG	4020
333	GACTTGATGA	ACTGATCCCC	AAAATGCGTA	TCACCCCTGCC	GCTACGGCTA	TGGCGATACT	4080
335	CATTATTCTG	GATGCCAAAT	CGGCATAAAG	ACAAACTTTT	AGGTGAGCGA	CTACGACTGG	4140
337	CCCTGCAAGA	ACTGGGGCCG	GTTTGATCA	AGTTCGGGCA	AATGTTATCA	ACCCGCCGCG	4200
339	ATCTTTTTCC	ACCGCATATT	GCCGATCAGC	TGGCGTTATT	GCAGGACAAA	GTTGCTCCGT	4260
341	TTGATGGCAA	GCTGGCGAAG	CAGCAGATTG	AAGCTGCAAT	GGGCGGCTTG	CCGGTAGAAG	4320
343	CGTGGTTTGA	CGATTTTGAA	ATCAAGCCGC	TGGCTTCTGC	TTCTATCGCC	CAGGTTTATA	4380
345	CCGCGCGATT	GAAATCGAAT	GGTAAAGAGG	TGGTGATTAA	AGTCATCCGC	CCGGATATTT	4440
347	TGCCGTTTAT	TAAAGCGGAT	CTGAACTTA	TCTACCGTCT	GGCTCGCTGG	GTGCCGCGTT	4500
349	TGCTGCCGGA	TGGTCGCCGT	CTGCGCCCAA	CCGAAGTG GT	GCGCGAGTAC	GAAAAGACAT	4560
351	TGATTGATGA	ACTGAATTTG	CTGCGGGAAT	CTGCCAACGC	CATTCAGCTT	CGGCGCAATT	4620
353	TTGAAGACAG	CCCGATGCTC	TACATCCCGG	AAGTTTACCC	TGACTATTGT	AGTGAAGGGA	4680
355	TGATGGTGAT	GGAGCGCATT	TACGGCATTC	CGGTGTCTGA	TGTTGCGGCG	CTGGAGAAAA	4740
357	ACGGCACTAA	CATGAAATTG	CTGGCGGAAC	GCGGCGTGCA	GGTGTCTTTC	ACTCAGGTCT	4800
359	TTGCGACAG	CTTTTTCCAT	GCCGATATGC	ACCCTGGCAA	CATCTTCGTA	AGCTATGAAC	4860
361	ACCCGAAAA	CCCGAAATAT	ATCGGCATTG	ATTGCGGGAT	TGTTGGCTCG	CTAAACAAAG	4920
363	AAGATAAACG	CTATCTGGCA	GAAAACTTTA	TGCGCTTCTT	TAATCGCGAC	TATCGCAAAG	4980
365	TGGCAGAGCT	ACACGTCGAT	TCTGGCTGGG	TGCCACCAGA	TACCAACGTT	GAAGAGTTTCG	5040
367	AATTTGCCAT	TCGTACGGTC	TGTGAACCTA	TCTTTGAGAA	ACCGCTGGCC	GAAATTTTCGT	5100
369	TTGGACATGT	ACTGTTAAAT	CTGTTTAAATA	CGGCGCGTCG	CTTCAATATG	GAAGTGCAGC	5160
371	CGCAACTGGT	GTTACTCCAG	AAAACCCCTGC	TCTACGTCGA	AGGGGTAGGA	CGCCAGCTTTT	5220
373	ATCCGCAACT	CGATTTATGG	AAAACGGCGA	AGCCTTTTCCT	GGAGTCGTGG	ATTAAAGATC	5280
375	AGGTCGGTAT	TCCTGCGCTG	GTGAGAGCAT	TTAAAGAAAA	AGCGCCGTTT	TGGGTCGAAA	5340
377	AAATGCCAGA	ACTGCCTGAA	TTGGTTTACG	ACAGTTTGCG	CCAGGGCAAG	TATTTACAGC	5400
379	ACAGTGTTGA	TAAGATTGCC	CGCGAGCTTC	AGTCAAATCA	TGTACGTCAG	GGACAATCGC	5460
381	GTTATTTTCT	CGGAATTGGC	GCTACGTTAG	TATTAAGTGG	CACATTCTTG	TTGGTCAGCC	5520
383	GACCTGAATG	GGGGCTGATG	CCCGGCTGGT	TAAATGGCAGG	TGGTCTGATC	GCCTGGTTTG	5580
385	TCGGTTGGCG	CAAAACACGC	TGATTTTTTC	ATCGCTCAAG	GCGGGCCGTG	TAACGTATAA	5640
387	TGCGGCTTTG	TTTAATCATC	ATCTACCACA	GAGGAACATG	TATGGGTGGT	ATCAGTATTT	5700
389	GGCAGTTATT	GATTATTGCC	GTCAATCGTTG	TACTGCTTTT	TGGCACCAAA	AAGCTCGGCT	5760
391	CCATCGGTTT	CGATCTTGGT	GCGTCGATCA	AAGGCTTTAA	AAAAGCAATG	AGCGATGATG	5820
393	AACCAAAGCA	GGATAAAACC	AGTCAGGATG	CTGATTTTAC	TGCGAAAAC	ATCGCCGATA	5880
395	AGCAGGCGGA	TACGAATCAG	GAACAGGCTA	AAACAGAAGA	CGCGAAGCGC	CACGATAAAG	5940
397	AGCAGGTGAA	TCCGTGTTTG	ATATCGGTTT	TAGCGAACTT	GCTATTGGTG	TTCATCATCG	6000
399	GCCTCGTCGT	TCTGGGGCCG	CAACGACTGC	CTGTGGCGGT	AAAAACGGTA	GCGGGCTGGA	6060
401	TTTCGCGCGTT	GCGTTCAC TG	GCGACAACGG	TGCAGAACGA	ACTGACCCAG	GAGTTAAAAC	6120
403	TCCAGGAGTT	TCAGGACAGT	CTGAAAAAGG	TTGAAAAAGC	GAGCCTCACT	AACCTGACGC	6180
405	CCGAAC TGAA	AGCGTCGATG	GATGAACTAC	GCCAGGCCGC	GGAGTCGATG	AAGCGTTTCCT	6240
407	ACGTTGCAAA	CGATCCTGAA	AAGGCGAGCG	ATGAAGCGCA	CACCATCCAT	AACCCGGTGG	6300
409	TGAAAGATAA	TGAAGCTGCG	CATGAGGGCG	TAACGCCTGC	CGCTGCACAA	ACGCAGGCCA	6360
411	GTTTCGCCGA	ACAGAAGCCA	GAAACCACGC	CAGAGCCGGT	GGTAAAACCT	GCTGCGGACG	6420
413	CTGAACCGAA	AACCGCTGCA	CTTCCCTTT	CGTCGAGTGA	TAAACCGTAA	ACATGCTCTGT	6480
415	AGAAGATACT	CAACCGCTTA	TCACGCATCT	GATTGAGCTG	CGTAAGCGTC	TGCTGAACTG	6540
417	CATTATCGCG	GTGATCGTGA	TATTCCTGTG	TCTGGTCTAT	TTCCGCAATG	ACATCTATCA	6600

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos.110
Seq#:7; Xaa Pos.61,62
Seq#:36; Xaa Pos.89

VERIFICATION SUMMARY

DATE: 05/01/2002

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Input Set : N:\Crf3\RULE60\10023171.raw

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:96

L:1088 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:48

L:2379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:80